

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,955

DATE: 07/27/2001

TIME: 19:56:41

Input Set : A:\78104023.app

Output Set: N:\CRF3\07272001\I806955.raw

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3 <110> APPLICANT: Panayi, Gabriel S
4 Corrigall, Valerie M
5 Bodman-Smith, Mark D
6 Fife, Mark S
7 Lanchbury, Jeremy S
9 <120> TITLE OF INVENTION: Treatment of Inflammatory Disease
11 <130> FILE REFERENCE: infection
13 <140> CURRENT APPLICATION NUMBER: 09/806955
14 <141> CURRENT FILING DATE: 2001-04-06
16 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03316
17 <151> PRIOR FILING DATE: 1999-10-08
19 <150> PRIOR APPLICATION NUMBER: GB9822115.3
20 <151> PRIOR FILING DATE: 1998-10-09
22 <160> NUMBER OF SEQ ID NOS: 5
24 <170> SOFTWARE: PatentIn Ver. 2.0
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27 <211> LENGTH: 639
28 <212> TYPE: PRT
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39 35 40 45
41 Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
42 50 55 60
44 Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
45 65 70 75 80
47 Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
48 85 90 95
50 Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
51 100 105 110
53 Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
54 115 120 125
56 Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
57 130 135 140
59 Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
60 145 150 155 160
62 Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn
63 165 170 175
65 Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly
66 180 185 190
68 Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
69 195 200 205
71 Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe

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72      210      215      220
74 Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
75 225      230      235      240
77 Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
78      245      250      255
80 Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
81      260      265      270
83 Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
84      275      280      285
86 Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu
87      290      295      300
89 Thr Arg Ala Lys Phe Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
90 305      310      315      320
92 Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
93      325      330      335
95 Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
96      340      345      350
98 Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro Ser Arg
99      355      360      365
101 Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
102      370      375      380
104 Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
105 385      390      395      400
107 Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
108      405      410      415
110 Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
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113 Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys Val Tyr
114      435      440      445
116 Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly Thr Phe
117      450      455      460
119 Asp Leu Thr Gly Ile Pro Ala Pro Arg Gly Val Pro Gln Ile Glu
120 465      470      475      480
122 Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr Ala Glu
123      485      490      495
125 Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
126      500      505      510
128 Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
129      515      520      525
131 Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
132      530      535      540
134 Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp
135 545      550      555      560
137 Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu Thr Met
138      565      570      575
140 Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His Gln Asp
141      580      585      590
143 Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu Glu Ile
144      595      600      605

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146 Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro Pro Pro
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149 Thr Gly Glu Glu Asp Thr Ala Glu Leu His His His His His His
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154 <211> LENGTH: 633
155 <212> TYPE: PRT
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162 Leu Gly Thr Thr Tyr Ser Cys Val Gly Val Phe Lys Asn Gly Arg Val
163      20          25          30
165 Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser Tyr Val
166      35          40          45
168 Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala Lys Asn
169      50          55          60
171 Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys Arg Leu
172  65          70          75          80
174 Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile Lys Phe
175      85          90          95
177 Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile Gln Val
178      100         105         110
180 Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu Ile Ser
181      115         120         125
183 Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr Leu Gly
184      130         135         140
186 Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe Asn Asp
187 145         150         155         160
189 Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly Leu Asn
190      165         170         175
192 Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr Gly
193      180         185         190
195 Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp Leu Gly
196      195         200         205
198 Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly Val Phe
199      210         215         220
201 Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu Asp Phe
202 225         230         235         240
204 Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys Lys Thr
205      245         250         255
207 Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu Arg Arg
208      260         265         270
210 Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln Ala Arg
211      275         280         285
213 Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu Thr Leu
214      290         295         300
216 Thr Arg Ala Lys Phe Glu Leu Asn Met Asp Leu Phe Arg Ser Thr
217 305         310         315         320

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219 Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys Lys Ser
220           325           330           335
222 Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile Pro Lys
223           340           345           350
225 Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro Ser Arg
226           355           360           365
228 Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val Gln Ala
229           370           375           380
231 Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu Leu Asp
232 385           390           395           400
234 Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val Met Thr
235           405           410           415
237 Lys Leu Ile Pro Arg Asn Thr Val Val Pro Thr Lys Lys Ser Gln Ile
238           420           425           430
240 Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys Val Tyr
241           435           440           445
243 Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly Thr Phe
244           450           455           460
246 Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu
247 465           470           475           480
249 Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr Ala Glu
250           485           490           495
252 Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn Asp Gln
253           500           505           510
255 Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp Ala Glu
256           515           520           525
258 Lys Phe Ala Glu Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp Thr Arg
259           530           535           540
261 Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile Gly Asp
262 545           550           555           560
264 Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu Thr Met
265           565           570           575
267 Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His Gln Asp
268           580           585           590
270 Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu Glu Ile
271           595           600           605
273 Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro Pro Pro
274           610           615           620
276 Thr Gly Glu Glu Asp Thr Ala Glu Leu
277 625           630
280 <210> SEQ ID NO: 3
281 <211> LENGTH: 1917
282 <212> TYPE: DNA
283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 3
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288 aaccgcatca cgccgtccta tgcgccttc actcctgaag gggaacgtct gattggcgat 180
289 gccgccaaga accagctcac ctccaacccc gagaacacgg tctttgacgc caagcggctc 240

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290 atcggccgca cgtggaatga cccgtctgtg cagcaggaca tcaagttctt gccgttcaag 300
291 gtgggttgaag agaaaactaa accatacatt caagttgata ttggaggtgg gcaaacaaag 360
292 acatttgctc ctgaagaaat ttctgccatg gttctcacta aaatgaaaga aaccgctgag 420
293 gcttattttg gaaagaaggt taccatgca gttgttactg taccagccta ttttaattgat 480
294 gcccacgccc aagcaaccaa agacgctgga actattgctg gcctaaatgt tatgaggatc 540
295 atcaacgagc ctacggcagc tgctattgct tatggcctgg ataagaggga gggggagaag 600
296 aacatcctgg tgtttgacct ggggtgcccga acctcgatg tgtctcttct caccattgac 660
297 aatggtgtct tcgaagttgt ggccactaat ggagatactc atctgggtgg agaagacttt 720
298 gaccagcgtg tcatggaaca ctcatcaaaa ctgtacaaaa agaagacggg caaagatgtc 780
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301 tctgagaccc tgactcgggc caaatttgaa gagctcaaca tggatctgtt ccggtctact 960
302 atgaagcccg tccagaaagt gttggaagat tctgatttga agaagtctga tattgatgaa 1020
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304 ttcaatggca aggaaccatc ccgtggcata aaccagatg aagctgtagc gtatgggtgt 1140
305 gctgtccagg ctggtgtgct ctctggtgat caagatacag gtgacctggg actgcttgat 1200
306 gtatgtcccc ttacacttgg tattgaaact gtgggaggtg tcatgaccaa actgattcca 1260
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311 gggaaacaaa ataagatcac aatcaccaat gaccagaatc gcctgacacc tgaagaaatc 1560
312 gaaaggatgg ttaatgatgc tgagaagttt gctgaggaag aaaaaagct caaggagcgc 1620
313 attgatacta gaaatgagtt ggaaagctat gcctattctc taaagaatca gattggagat 1680
314 aaagaaaagc tgggaggtaa actttcctct gaagataagg agaccatgga aaaagctgta 1740
315 gaagaaaaga ttgaatggct ggaaagccac caagatgctg acattgaaga cttcaaagct 1800
316 aagaagaagg aactggaaga aattgttcaa ccaattatca gcaaactcta tggaagtgca 1860
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319 <210> SEQ ID NO: 4

320 <211> LENGTH: 32

321 <212> TYPE: DNA

322 <213> ORGANISM: Artificial Sequence

324 <220> FEATURE:

325 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

327 <400> SEQUENCE: 4

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330 <210> SEQ ID NO: 5

331 <211> LENGTH: 32

332 <212> TYPE: DNA

333 <213> ORGANISM: Artificial Sequence

335 <220> FEATURE:

336 <223> OTHER INFORMATION: Description of Artificial Sequence: primer

338 <400> SEQUENCE: 5

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/806,955

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